

SEQUENCE LISTINGS

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: COOPERATIVE RESEARCH CENTRE FOR TROPICAL PLANT
PATHOLOGY

(B) STREET: The University of Queensland

(C) CITY: St Lucia

(D) STATE: Queensland

(E) COUNTRY: Australia

(F) POSTAL CODE (ZIP): 4067

(ii) TITLE OF INVENTION: Antimicrobial Protein

(iii) NUMBER OF SEQUENCES: 28

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Macadamia integrifolia

(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
1 5 10 15

Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
20 25 30

Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
35 40 45

Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
50 55 60

Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr

35

	65		70		75		80
	Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro	85		90		95	
5	Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu	100		105		110	
	Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln	115		120		125	
10	Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln	130		135		140	
	Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys	145		150		155	160
	Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr	165		170		175	
20	Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg	180		185		190	
	Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln	195		200		205	
	Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly	210		215		220	
30	Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr	225		230		235	240
	Glu Glu Gly Glu Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu	245		250		255	
35	Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val	260		265		270	
	Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn	275		280		285	
40	Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro	290		295		300	
	Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly	305		310		315	320
	Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu	325		330		335	
50	Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile	340		345		350	
	Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr	355		360		365	
55							

66250:TESFEED

36

Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 370 375 380
 5 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 385 390 395 400
 Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
 405 410 415
 10 Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Glu Leu
 420 425 430
 Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
 435 440 445
 15 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460
 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 465 470 475 480
 Gln Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Thr Gln
 485 490 495
 25 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 500 505 510
 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
 515 520 525
 30 Ser Gly Arg His Gly Gly Arg Gly Gly Gly Lys Arg His Glu Glu Glu
 530 535 540
 Glu Asp Val His Tyr Glu Gln Val Arg Ala Arg Leu Ser Lys Arg Glu
 545 550 555 560
 Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
 565 570 575
 40 Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
 580 585 590
 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
 595 600 605
 45 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
 610 615 620
 Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
 625 630 635 640
 Arg Gln His Gln Gln Gln Ser Pro Arg Ser Thr Lys Gln Gln Gln Pro
 645 650 655
 55 Leu Val Ser Ile Leu Asp Phe Val Gly Phe
 660 665

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Macadamia integrifolia*
15 (F) TISSUE TYPE: Seeds

- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:1..85
- 20

- (x) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:86..1999
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTTCACT CTCCTTCTG 60

30 TCTACGACAG TGTCTCTTGC TGAAAGTGAA TTTGACAGGC AGGAATATGA GGAGTGCAAA 120

CGGCAATGCA TGCAGTTGGA GACATCAGGC CAGATGCGTC GGTGTGTGAG TCACTGCGAT 180

AAGAGATTTG AAGAGGATAT AGATTGGTCT AAGTATGATA ACCAAGAGGA TCCTCAGACG 240

35 GAATGCCAAC AATGCCAGAG GCGATGCAGG CAGCAGGAGA GTGGCCCACG TCAGCAACAA 300

TACTGCCAAC GACGCTGCAA GGAAATATGT GAAGAAGAAG AAGAATATAA CCGACAACGT 360

40 GATCCACAGC AGCAATACGA GCAATGTCAG AAGCACTGCC AACGGCGCGA GACAGAGCCA 420

CGTCACATGC AAACATGTCA ACAACGCTGC GAGAGGAGAT ATGAAAAGGA GAAACGTAAG 480

CAACAAAAGA GATATGAAGA GCAACAACGT GAAGACGAAG AGAAATATGA AGAGCGAATG 540

45 AAGGAAGAAG ATAACAAACG CGATCCACAA CAAAGAGAGT ACGAAGACTG CCGGAGGCGC 600

TGCGAACAAC AGGAGCCACG TCAGCAGCAC CAGTGCCAGC TAAGATGCCG AGAGCAGCAG 660

50 AGGCAACACG GCCGAGGTGG CGATATGATG AACCTCAGA GGGGAGGCAG CGGCAGATAC 720

GAGGAGGGAG AAGAGGAGCA AAGCGACAAC CCCTACTACT TCGACGAACG AAGCTTAAGT 780

ACAAGGTTCA GGACCGAGGA AGGCCACATC TCAGTTCTGG AGAACTTCTA TGGTAGATCC 840

55 AAGCTTCTAC GCGCACTAAA AACTATCGC TTGGTGCTCC TCGAGGCTAA CCCCACGCC 900

TTCTGCTCC CTACCCACTT GGATGCAGAT GCCATTCTCT TGGTCATAGG AGGGAGAGGA 960
5 GCCCTCAAAA TGATCCACCA CGACAACAGA GAATCCTACA ACCTCGAGTG TGGAGACGTA 1020
ATCAGAATCC CAGCTGGAAC CACATTCTAC TTAATCAACC GAGACAACAA CGAGAGGCTC 1080
CACATAGCCA AGTTCTTACA GACCATATCC ACTCCTGGCC AATACAAGGA ATTCTTCCCA 1140
10 GCTGGAGGCC AAAACCCAGA GCCGTACCTC AGTACCTTCA GCAAAGAGAT TCTCGAGGCT 1200
GCGCTCAACA CACAAACAGA GAAGCTGCGT GGGGTGTTTG GACAGCAAAG GGAGGGAGTG 1260
ATAATTAGGG CGTCACAGGA GCAGATCAGG GAGTTGACTC GAGATGACTC AGAGTCACGA 1320
15 CACTGGCATA TAAGGAGAGG TGGTGAATCA AGCAGGGGAC CTTACAATCT GTTCAACAAA 1380
AGGCCACTGT ACTCCAACAA ATACGGTCAA GCCTACGAAG TCAAACCTGA GGACTACAGG 1440
20 CAACTCCAAG ACATGGACTT ATCGGTTTTT ATAGCCAACG TCACCCAGGG ATCCATGATG 1500
GGTCCCTTCT TCAACACTAG GTCTACAAAG GTGGTAGTGG TGGCTAGTGG AGAGGCAGAT 1560
GTGGAAATGG CATGCCCTCA CTTGTCGGGA AGACACGGCG GCCGCGGTGG AGGAAAAAGG 1620
25 CATGAGGAGG AAGAGGATGT GCACTATGAG CAGGTTAGAG CACGTTTGTC GAAGAGAGAG 1680
GCCATTGTTG TTCTGGCAGG TCATCCCGTC GTCTTCGTTT CATCCGGAAA CGAGAACCTG 1740
30 CTGCTTTTTT CATTGTGAAT CAATGCCCAA AACAACCACG AGAACTTCCT CGCGGGGAGA 1800
GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA 1860
AGGAAAGAGG TAGAAGAGTC ATTTAACAGC CAGGACCAGT CTATCTTCTT TCCTGGGCCC 1920
35 AGGCAGCACC AGCAACAGTC GCCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT 1980
CTGGAATTCT TTGGCTTCTA AAGTTCCACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG 2040
40 TAGCTCCTAG CTCGGTGTAT GAGAGTGGTA AGAGACTAAG ACGCTAAATC CCTAAGTAAC 2100
TAACCTGGCG AGCTTGCGTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA 2160
45 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Macadamia integrifolia*
 (F) TISSUE TYPE: Seeds

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION:1..28

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:29..666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Ala	Ile	Asn	Thr	Ser	Asn	Leu	Cys	Ser	Leu	Leu	Phe	Leu	Leu	Ser	1	5	10	15
Leu	Phe	Leu	Leu	Ser	Thr	Thr	Val	Ser	Leu	Ala	Glu	Ser	Glu	Phe	Asp	20	25	30	
Arg	Gln	Glu	Tyr	Glu	Glu	Cys	Lys	Arg	Gln	Cys	Met	Gln	Leu	Glu	Thr	35	40	45	
Ser	Gly	Gln	Met	Arg	Arg	Cys	Val	Ser	Gln	Cys	Asp	Lys	Arg	Phe	Glu	50	55	60	
Glu	Asp	Ile	Asp	Trp	Ser	Lys	Tyr	Asp	Asn	Gln	Asp	Asp	Pro	Gln	Thr	65	70	75	80
Asp	Cys	Gln	Gln	Cys	Gln	Arg	Arg	Cys	Arg	Gln	Gln	Glu	Ser	Gly	Pro	85	90	95	
Arg	Gln	Gln	Gln	Tyr	Cys	Gln	Arg	Arg	Cys	Lys	Glu	Ile	Cys	Glu	Glu	100	105	110	
Glu	Glu	Glu	Tyr	Asn	Arg	Gln	Arg	Asp	Pro	Gln	Gln	Gln	Tyr	Glu	Gln	115	120	125	
Cys	Gln	Glu	Arg	Cys	Gln	Arg	His	Glu	Thr	Glu	Pro	Arg	His	Met	Gln	130	135	140	
Thr	Cys	Gln	Gln	Arg	Cys	Glu	Arg	Arg	Tyr	Glu	Lys	Glu	Lys	Arg	Lys	145	150	155	160
Gln	Gln	Lys	Arg	Tyr	Glu	Glu	Gln	Gln	Arg	Glu	Asp	Glu	Glu	Lys	Tyr	165	170	175	
Glu	Glu	Arg	Met	Lys	Glu	Glu	Asp	Asn	Lys	Arg	Asp	Pro	Gln	Gln	Arg	180	185	190	
Glu	Tyr	Glu	Asp	Cys	Arg	Arg	Arg	Cys	Glu	Gln	Gln	Glu	Pro	Arg	Gln	195	200	205	
Gln	Tyr	Gln	Cys	Gln	Arg	Arg	Cys	Arg	Glu	Gln	Gln	Arg	Gln	His	Gly	210	215	220	

Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
 225 230 235 240
 5 Glu Glu Gly Glu Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
 245 250 255
 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
 260 265 270
 10 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
 275 280 285
 Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
 290 295 300
 15 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
 305 310 315 320
 20 Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
 325 330 335
 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
 340 345 350
 25 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
 355 360 365
 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 370 375 380
 30 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 385 390 395 400
 35 Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
 405 410 415
 Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
 420 425 430
 40 Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
 435 440 445
 45 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460
 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 465 470 475 480
 50 Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
 485 490 495
 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 500 505 510
 55 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu

41

515

520

525

Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
530 535 540

Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
545 550 555 560

Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
565 570 575

Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
580 585 590

His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
595 600 605

Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
610 615 620

Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
625 630 635 640

Arg Gln His Gln Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
645 650 655

Leu Val Ser Ile Leu Asp Phe Val Gly Phe
660 665

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macadamia integrifolia*
- (F) TISSUE TYPE: Seeds

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION:1..86

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:87..1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTTCCT CTCCTTCTG

60

	TCAACGACAG	TGTCTCTTGC	TGAAAGTGAA	TTTGACAGGC	AGGAATATGA	GGAGTGCAAA	120
5	CGGCAATGCA	TGCAGTTGGA	GACATCAGGC	CAGATGCGTC	GGTGTGTGAG	TCAGTGCGAT	180
	AAGAGATTTG	AAGAGGATAT	AGATTGGTCT	AAGTATGATA	ACCAAGACGA	TCCTCAGACG	240
	GATTGCCAAC	AATGCCAGAG	GCGATGCAGG	CAGCAGGAGA	GTGGCCCACG	TCAGCAACAA	300
10	TACTGCCAAC	GACGCTGCAA	GGAAATATGT	GAAGAAGAAG	AAGAATATAA	CCGACAACGT	360
	GATCCACAGC	AGCAATACGA	GCAATGTCAG	GAGCGCTGCC	AACGGCACGA	GACAGAGCCA	420
15	CGTCACATGC	AAACATGTCA	ACAACGCTGC	GAGAGGAGAT	ATGAAAAGGA	GAAACGTAAG	480
	CAACAAAAGA	GATATGAAGA	GCAACAACGT	GAAGACGAAG	AGAAATATGA	AGAGCGAATG	540
	AAGGAAGAAG	ATAACAAACG	CGATCCACAA	CAAAGAGAGT	ACGAAGACTG	CCGGAGGCGC	600
20	TGCGAACAAAC	AGGAGCCACG	TCAGCAGTAC	CAGTGCCAGC	GAAGATGCCG	AGAGCAGCAG	660
	AGGCAACACG	GCCGAGGTGG	TGATTTGATT	AACCCTCAGA	GGGGAGGCAG	CGGCAGATAC	720
25	GAGGAGGGAG	AAGAGAAGCA	AAGCGACAAC	CCCTACTACT	TCGACGAACG	AAGCTTAAGT	780
	ACAAGGTTCA	GGACCGAGGA	AGGCCACATC	TCAGTTCTGG	AGAACTTCTA	TGGTAGATCC	840
	AAGCTTCTAC	GCGCACTAAA	AAACTATCGC	TTGGTGCTCC	TCGAGGCTAA	CCCCAACGCC	900
30	TTCGTGCTCC	CTACCCACTT	GGACGCAGAT	GCCATTCTCT	TGGTCACCGG	AGGGAGAGGA	960
	GCCCTCAAAA	TGATCCACCG	TGACAACAGA	GAATCCTACA	ACCTCGAGTG	TGGAGACGTA	1020
35	ATCAGAATCC	CAGCTGGAAC	CACATTCTAC	TTAATCAACC	GAGACAACAA	CGAGAGGCTC	1080
	CACATAGCCA	AGTTCTTACA	GACCATATCC	ACTCCTGGCC	AATACAAGGA	ATTCTTCCCA	1140
	GCTGGAGGCC	AAAACCCAGA	GCCGTACCTC	AGTACCTTCA	GCAAAGAGAT	TCTCGAGGCT	1200
40	GCGCTCAACA	CACAAGCAGA	GAGGCTGCGT	GGGGTGCTTG	GACAGCAAAG	GGAGGGAGTG	1260
	ATAATTAGTG	CGTCACAGGA	GCAGATCAGG	GAGTTGACTC	GAGATGACTC	AGAGTCACGA	1320
45	CGCTGGCATA	TAAGGAGAGG	TGGTGAATCA	AGCAGGGGAC	CTTACAATCT	GTTCAACAAA	1380
	AGGCCACTGT	ACTCCAACAA	ATACGGTCAA	GCCTACGAAG	TCAAACCTGA	GGACTACAGG	1440
	CAACTCCAAG	ACATGGACGT	ATCGGTTTTT	ATAGCCAACA	TCACCCAGGG	ATCCATGATG	1500
50	GGTCCCTTCT	TCAACACTAG	GTCTACAAAG	GTGGTAGTGG	TGGCTAGTGG	AGAGGCAGAT	1560
	GTGGAAATGG	CATGCCCTCA	CTTGTCGGGA	AGACACGGCG	GCCGCCGTGG	AGGGAAAAGG	1620
55	CATGAGGAGG	AAGAGGATGT	GCACTATGAG	CAGGTTAAAG	CACGTTTGTC	GAAGAGAGAG	1680
	GCCATTGTTG	TTCCGGTAGG	TCATCCCGTC	GTCTTCGTTT	CATCCGAAA	CGAGAACCTG	1740

CTGCTTTTTG CATTTGGAAT CAATGCCCAA AACAACCACG AGAACTTCCT CGCGGGGAGA 1800
5 GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA 1860
AGGAAAGAGG TAGAAGAGTT ATTTAACAGC CAGGACGAGT CTATCTTCTT TCCTGGGCCC 1920
AGGCAGCACC AGCAACAGTC TTCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT 1980
10 CTGGACTTCG TTGGCTTCTA AAGTTCTACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG 2040
TAGCTCCTAG CTCGGTGTAT GCGAGTGGTA AGAGACCAAG ACGCTAAATC CCTAAGTAAC 2100
TAACCTGGCG AGCTTGCGTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA 2160
15 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macadamia integrifolia*
(F) TISSUE TYPE: Seeds

(ix) FEATURE:

- (A) NAME/KEY: partial mat_peptide
(B) LOCATION:1..625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Cys Met Gln Leu Glu Thr Ser Gly Gln Met Arg Arg Cys Val Ser
1 5 10 15
Gln Cys Asp Lys Arg Phe Glu Glu Asp Ile Asp Trp Ser Lys Tyr Asp
20 25 30
Asn Gln Glu Asp Pro Gln Thr Glu Cys Gln Gln Cys Gln Arg Arg Cys
35 40 45
Arg Gln Gln Glu Ser Asp Pro Arg Gln Gln Gln Tyr Cys Gln Arg Arg
50 55 60
Cys Lys Glu Ile Cys Glu Glu Glu Glu Tyr Asn Arg Gln Arg Asp
65 70 75 80
Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu
85 90 95

44

	Thr	Glu	Pro	Arg	His	Met	Gln	Ile	Cys	Gln	Gln	Arg	Cys	Glu	Arg	Arg	
						100				105					110		
5	Tyr	Glu	Lys	Glu	Lys	Arg	Lys	Gln	Gln	Lys	Arg	Tyr	Glu	Glu	Gln	Gln	
			115					120					125				
	Arg	Glu	Asp	Glu	Glu	Lys	Tyr	Glu	Glu	Arg	Met	Lys	Glu	Gly	Asp	Asn	
			130				135					140					
10	Lys	Arg	Asp	Pro	Gln	Gln	Arg	Glu	Tyr	Glu	Asp	Cys	Arg	Arg	His	Cys	
	145					150					155					160	
	Glu	Gln	Gln	Glu	Pro	Arg	Leu	Gln	Tyr	Gln	Cys	Gln	Arg	Arg	Cys	Gln	
15	165				170					175					180		
	Glu	Gln	Gln	Arg	Gln	His	Gly	Arg	Gly	Gly	Asp	Leu	Met	Asn	Pro	Gln	
				185					190					195			
20	Arg	Gly	Gly	Ser	Gly	Arg	Tyr	Glu	Glu	Gly	Glu	Glu	Lys	Gln	Ser	Asp	
			200					205					210				
	Asn	Pro	Tyr	Tyr	Phe	Asp	Glu	Arg	Ser	Leu	Ser	Thr	Arg	Phe	Arg	Thr	
		215					220					225					
25	Glu	Glu	Gly	His	Ile	Ser	Val	Leu	Glu	Asn	Phe	Tyr	Gly	Arg	Ser	Lys	
	230				235						240					245	
	Leu	Leu	Arg	Ala	Leu	Lys	Asn	Tyr	Arg	Leu	Val	Leu	Leu	Glu	Ala	Asn	
30					250					255					260		
	Pro	Asn	Ala	Phe	Val	Leu	Pro	Thr	His	Leu	Asp	Ala	Asp	Ala	Ile	Leu	
			265					270						275			
35	Leu	Val	Ile	Gly	Gly	Arg	Gly	Ala	Leu	Lys	Met	Ile	His	Arg	Asp	Asn	
		280					285						290				
	Arg	Glu	Ser	Tyr	Asn	Leu	Glu	Cys	Gly	Asp	Val	Ile	Arg	Ile	Pro	Ala	
		295				300						305					
40	Gly	Thr	Thr	Phe	Tyr	Leu	Ile	Asn	Arg	Asp	Asn	Asn	Glu	Arg	Leu	His	
	310					315					320				325		
	Ile	Ala	Lys	Phe	Leu	Gln	Thr	Ile	Ser	Thr	Pro	Gly	Gln	Tyr	Lys	Glu	
45					330					335					340		
	Phe	Phe	Pro	Ala	Gly	Gly	Gln	Asn	Pro	Glu	Pro	Tyr	Leu	Ser	Thr	Phe	
				345				350						355			
50	Ser	Lys	Glu	Ile	Leu	Glu	Ala	Ala	Leu	Asn	Thr	Gln	Thr	Glu	Arg	Leu	
		360					365						370				
	Arg	Gly	Val	Leu	Gly	Gln	Gln	Arg	Glu	Gly	Val	Ile	Ile	Arg	Ala	Ser	
		375				380						385					
55	Gln	Glu	Gln	Ile	Arg	Glu	Leu	Thr	Arg	Asp	Asp	Ser	Glu	Ser	Arg	Arg	
	390					395				400						405	

[illegible]

10 Phe Ile Ala Asn Ile Thr Gln Gly Ser Met Met Gly Pro Phe Phe Asn
455 460 470

15																			
	480					485				490									500
	Glu	Met	Ala	Cys	Pro	His	Leu	Ser	Gly	Arg	His	Gly	Gly	Arg	Gly	Gly			
					505					510					515				

20 Gly Lys Arg His Glu Glu Glu Glu Glu Val His Tyr Glu Gln Val Arg
520 525 530

25

Val Val Phe Val Ser Ser Gly Asn Glu Asn Leu Leu Leu Phe Ala Phe

550 555 560

30 Gly Ile Asn Ala Gln Asn Asn His Glu Asn Phe Leu Ala Gly Arg Glu
565 570 575 580

Arg Asn Val Leu Gln Gln Ile Glu Pro Gln Ala Met Glu Leu Ala Phe
585 590 595

600 605 610

Ser Ile Phe Phe Pro Gly Pro Arg Gln His Gln Gln Gln Ser Pro Arg

615 620 625

40

Ser Thr Lys Gln Gln Gln Pro Leu Val Ser Ile Leu Asp Phe Val Gly
630 635 640

Phe

Ser Thr Lys Gln Gln Gln Pro Leu Val Ser Ile Leu Asp Phe Val Gly
630 635 640
Phe

45 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Macadamia integrifolia*

(F) TISSUE TYPE: Seeds

(x) FEATURE:

(A) NAME/KEY: partial mat_peptide

(B) LOCATION:1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10	CAATGCATGC AGTTAGAGAC ATCAGGCCAG ATGCGTCGGT GTGTGAGTCA GTGCGATAAG	60
	AGATTTGAAG AGGATATAGA TTGGTCTAAG TATGATAACC AAGAGGATCC TCAGACGGAA	120
	TGCCAACAAT GCCAGAGGCG ATGCAGGCAG CAGGAGAGTG ACCCACGTCA GCAACAATAC	180
15	TGCCAACGAC GCTGCAAGGA AATATGTGAA GAAGAAGAAG AATATAACCG ACAACGTGAT	240
	CCACAGCAGC AATACGAGCA ATGTCAGAAG CGCTGCCAAC GGCGCGAGAC AGAGCCACGT	300
20	CACATGCAAA TATGTCAACA ACGCTGCGAG AGGAGATATG AAAAGGAGAA ACGTAAGCAA	360
	CAAAAGAGAT ATGAAGAGCA ACAACGTGAA GACGAAGAGA AATATGAAGA GCGAATGAAG	420
	GAAGGAGATA ACAAACGCGA TCCACAACAA AGAGAGTACG AAGACTGCCG GCGGCACTGC	480
25	GAACAACAGG AGCCACGTCT GCAGTACCAG TGCCAGCGAA GATGCCAAGA GCAGCAGAGG	540
	CAACACGGCC GAGGTGGCGA TTTGATGAAC CCTCAGAGGG GAGGCAGCGG CAGATACGAG	600
	GAGGGAGAAG AGAAGCAAAG CGACAACCCC TACTACTTCG ACGAACGAAG CTTAAGTACA	660
30	AGGTTTCAGGA CCGAGGAAGG CCACATCTCA GTTCTGGAGA ACTTCTATGG TAGATCCAAG	720
	CTTCTACGCG CACTAAAAAA CTATCGCTTG GTGCTCCTCG AGGCTAACCC CAACGCCTTC	780
35	GTGCTCCCTA CCCACTTGGA TGCAGATGCC ATTCTCTTGG TCATCGGAGG GAGAGGAGCC	840
	CTCAAAATGA TCCACCGTGA CAACAGAGAA TCCTACAACC TCGAGTGTGG AGACGTAATC	900
	AGAATCCCAG CTGGAACCAC ATTCTACTTA ATCAACCGAG ACAACAACGA GAGGCTCCAC	960
40	ATAGCCAAGT TCTTACAGAC CATATCCACT CCTGGCCAAT ACAAGGAATT CTTCCCAGCT	1020
	GGAGGCCAAA ACCCAGAGCC GTACCTCAGT ACCTTCAGCA AAGAGATTCT CGAGGCTGCG	1080
45	CTCAACACAC AAACAGAGAG GCTGCGTGGG GTGCTTGGAC AGCAAAGGGA GGGAGTGATA	1140
	ATTAGGGCGT CACAGGAGCA GATCAGGGAG TTGACTCGAG ATGACTCAGA GTCACGACGC	1200
	TGGCATATAA GGAGAGGTGG TGAATCAAGC AGGGGACCTT ACAATCTGTT CAACAAAAGG	1260
50	CCACTGTACT CCAACAAATA CGGTCAAGCC TACGAAGTCA AACCTGAGGA CTACAGGCAA	1320
	CTCCAAGACA TGGACGTATC AGTTTTTCATA GCCAACATCA CCCAGGGATC CATGATGGGT	1380
55	CCCTTCTTCA AACTAGGTC TACAAAGGTG GTAGTGGTGG CTAGTGGAGA GGCAGATGTG	1440

GAAATGGCAT GCCCTCACTT GTCGGGAAGA CACGGCGGCC GCGGTGGAGG GAAAAGGCAT 1500
 GAGGAGGAAG AGGAGGTGCA CTATGAGCAG GTTAGAGCAC GTTTGTCGAA GAGAGAGGCC 1560
 5 ATTGTTGTTT TGGCAGGTCA TCCCGTCGTC TTCGTTTCAT CCGGAAACGA AAACCTGCTG 1620
 CTTTTTGCAT TTGGAATCAA TGCCCAAAAC AACCACGAGA ACTTCCTCGC GGGGAGAGAG 1680
 10 AGGAACGTGC TGCAGCAGAT AGAGCCACAG GCAATGGAGC TAGCGTTTGC CGCTTCAAGG 1740
 AAAGAGGTAG AAGAGTTATT TAACAGCCAG GACGAGTCTA TCTTCTTTCC TGGGCCCAGG 1800
 CAGCACCAGC AACAGTCGCC CCGCTCCACC AAGCAACAAC AGCCTCTCGT CTCCATTCTG 1860
 15 GACTTCGTTG GCTTCTAAAG TTCTACAAAA AAGAGTGTGT TATGTAGTAT AGGTTAGTAG 1920
 CTCCTAGCTC GGTGTATGAG AGTGGTAAGA GACTAAGACG CTAAATCCCT AAGTAACTAA 1980
 20 CCTGGCGAGC TTGCGTGTAT GCAAATAAAG AGGAACAGCT TTCCAACCTT AGAAAGCTCT 2040
 TTTTTTTTTT TTTTTTCTTT CTTTTTCTTA AGAAATAAAC GAACGTAGAT TGCGGCTCAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2140

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Theobroma cacao
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Val Ile Ser Lys Ser Pro Phe Ile Val Leu Ile Phe Ser Leu Leu
 1 5 10 15
 45 Leu Ser Phe Ala Leu Leu Cys Ser Gly Val Ser Ala Tyr Gly Arg Lys
 20 25 30
 Gln Tyr Glu Arg Asp Pro Arg Gln Gln Tyr Glu Gln Cys Gln Arg Arg
 35 40 45
 50 Cys Glu Ser Glu Ala Thr Glu Glu Arg Glu Gln Glu Gln Cys Glu Gln
 50 55 60
 55 Arg Cys Glu Arg Glu Tyr Lys Glu Gln Gln Arg Gln Gln Glu Glu Glu
 65 70 75 80

48

Leu Gln Arg Gln Tyr Gln Gln Cys Gln Gly Arg Cys Gln Glu Gln Gln
 85 90 95
 5 Gln Gly Gln Arg Glu Gln Gln Gln Cys Gln Arg Lys Cys Trp Glu Gln
 100 105 110
 Tyr Lys Glu Gln Glu Arg Gly Glu His Glu Asn Tyr His Asn His Lys
 115 120 125
 10 Lys Asn Arg Ser Glu Glu Glu Glu Gly Gln Gln Arg Asn Asn Pro Tyr
 130 135 140
 Tyr Phe Pro Lys Arg Arg Ser Phe Gln Thr Arg Phe Arg Asp Glu Glu
 145 150 155 160
 15 Gly Asn Phe Lys Ile Leu Gln Arg Phe Ala Glu Asn Ser Pro Pro Leu
 165 170 175
 Lys Gly Ile Asn Asp Tyr Arg Leu Ala Met Phe Glu Ala Asn Pro Asn
 180 185 190
 20 Thr Phe Ile Leu Pro His His Cys Asp Ala Glu Ala Ile Tyr Phe Val
 195 200 205
 25 Thr Asn Gly Lys Gly Thr Ile Thr Phe Val Thr His Glu Asn Lys Glu
 210 215 220
 Ser Tyr Asn Val Gln Arg Gly Thr Val Val Ser Val Pro Ala Gly Ser
 225 230 235 240
 30 Thr Val Tyr Val Val Ser Gln Asp Asn Gln Glu Lys Leu Thr Ile Ala
 245 250 255
 Val Leu Ala Leu Pro Val Asn Ser Pro Gly Lys Tyr Glu Leu Phe Phe
 260 265 270
 Pro Ala Gly Asn Asn Lys Pro Glu Ser Tyr Tyr Gly Ala Phe Ser Tyr
 275 280 285
 40 Glu Val Leu Glu Thr Val Phe Asn Thr Gln Arg Glu Lys Leu Glu Glu
 290 295 300
 Ile Leu Glu Glu Gln Arg Gly Gln Lys Arg Gln Gln Gly Gln Gln Gly
 305 310 315 320
 45 Met Phe Arg Lys Ala Lys Pro Glu Gln Ile Arg Ala Ile Ser Gln Gln
 325 330 335
 Ala Thr Ser Pro Arg His Arg Gly Gly Glu Arg Leu Ala Ile Asn Leu
 340 345 350
 Leu Ser Gln Ser Pro Val Tyr Ser Asn Gln Asn Gly Arg Phe Phe Glu
 355 360 365
 55 Ala Cys Pro Glu Asp Phe Ser Gln Phe Gln Asn Met Asp Val Ala Val
 370 375 380

Ser Ala Phe Lys Leu Asn Gln Gly Ala Ile Phe Val Pro His Tyr Asn
 385 390 395 400
 5 Ser Lys Ala Thr Phe Val Val Phe Val Thr Asp Gly Tyr Gly Tyr Ala
 405 410 415
 Gln Met Ala Cys Pro His Leu Ser Arg Gln Ser Gln Gly Ser Gln Ser
 420 425 430
 10 Gly Arg Gln Asp Arg Arg Glu Gln Glu Glu Glu Ser Glu Glu Glu Thr
 435 440 445
 Phe Gly Glu Phe Gln Gln Val Lys Ala Pro Leu Ser Pro Gly Asp Val
 450 455 460
 15 Phe Val Ala Pro Ala Gly His Ala Val Thr Phe Phe Ala Ser Lys Asp
 465 470 475 480
 20 Gln Pro Leu Asn Ala Val Ala Phe Gly Leu Asn Ala Gln Asn Asn Gln
 485 490 495
 Arg Ile Phe Leu Ala Gly Arg Pro Phe Phe Leu Asn His Lys Gln Asn
 500 505 510
 25 Thr Asn Val Ile Lys Phe Thr Val Lys Ala Ser Ala Tyr
 515 520 525

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gossypium hirsutum*
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Val Arg Asn Lys Ser Ala Cys Val Val Leu Leu Phe Ser Leu Phe
 1 5 10 15
 Leu Ser Phe Gly Leu Leu Cys Ser Ala Lys Asp Phe Pro Gly Arg Arg
 20 25 30
 Gly Asp Asp Asp Pro Pro Lys Arg Tyr Glu Asp Cys Arg Arg Arg Cys
 35 40 45
 55 Glu Trp Asp Thr Arg Gly Gln Lys Glu Gln Gln Gln Cys Glu Glu Ser
 50 55 60

Cys Lys Ser Gln Tyr Gly Glu Lys Asp Gln Gln Gln Arg His Arg Pro
 65 70 75 80
 5 Glu Asp Pro Gln Arg Arg Tyr Glu Glu Cys Gln Gln Glu Cys Arg Gln
 85 90 95
 Gln Glu Glu Arg Gln Gln Pro Gln Cys Gln Gln Arg Cys Leu Lys Arg
 100 105 110
 10 Phe Glu Gln Glu Gln Gln Gln Ser Gln Arg Gln Phe Gln Glu Cys Gln
 115 120 125
 Gln His Cys His Gln Gln Glu Gln Arg Pro Glu Lys Lys Gln Gln Cys
 130 135 140
 15 Val Arg Glu Cys Arg Glu Lys Tyr Gln Glu Asn Pro Trp Arg Gly Glu
 145 150 155 160
 20 Arg Glu Glu Glu Ala Glu Glu Glu Glu Thr Glu Glu Gly Glu Gln Glu
 165 170 175
 Gln Ser His Asn Pro Phe His Phe His Arg Arg Ser Phe Gln Ser Arg
 180 185 190
 25 Phe Arg Glu Glu His Gly Asn Phe Arg Val Leu Gln Arg Phe Ala Ser
 195 200 205
 Arg His Pro Ile Leu Arg Gly Ile Asn Glu Phe Arg Leu Ser Ile Leu
 210 215 220
 Glu Ala Asn Pro Asn Thr Phe Val Leu Pro His His Cys Asp Ala Glu
 225 230 235 240
 35 Lys Ile Tyr Leu Val Thr Asn Gly Arg Gly Thr Leu Thr Phe Leu Thr
 245 250 255
 His Glu Asn Lys Glu Ser Tyr Asn Ile Val Pro Gly Val Val Val Lys
 260 265 270
 40 Val Pro Ala Gly Ser Thr Val Tyr Leu Ala Asn Gln Asp Asn Lys Glu
 275 280 285
 Lys Leu Ile Ile Ala Val Leu His Arg Pro Val Asn Asn Pro Gly Gln
 290 295 300
 Phe Glu Glu Phe Phe Pro Ala Gly Ser Gln Arg Pro Gln Ser Tyr Leu
 305 310 315 320
 50 Arg Ala Phe Ser Arg Glu Ile Leu Glu Pro Ala Phe Asn Thr Arg Ser
 325 330 335
 Glu Gln Leu Asp Glu Leu Phe Gly Gly Arg Gln Ser Arg Arg Arg Gln
 340 345 350
 55 Gln Gly Gln Gly Met Phe Arg Lys Ala Ser Gln Glu Gln Ile Arg Ala

51

355

360

365

5 Leu Ser Gln Glu Ala Thr Ser Pro Arg Glu Lys Ser Gly Glu Arg Phe
 370 375 380
 Ala Phe Asn Leu Leu Ser Gln Thr Pro Arg Tyr Ser Asn Gln Asn Gly
 385 390 395 400
 10 Arg Phe Phe Glu Ala Cys Pro Pro Glu Phe Arg Gln Leu Arg Asp Ile
 405 410 415
 Asn Val Thr Val Ser Ala Leu Gln Leu Asn Gln Gly Ser Ile Phe Val
 420 425 430
 15 Pro His Tyr Asn Ser Lys Ala Thr Phe Val Ile Leu Val Thr Glu Gly
 435 440 445
 Asn Gly Tyr Ala Glu Met Val Ser Pro His Leu Pro Arg Gln Ser Ser
 450 455 460
 20 Tyr Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Gln Glu Gln Glu
 465 470 475 480
 25 Glu Glu Arg Arg Ser Gly Gln Tyr Arg Lys Ile Arg Ser Arg Leu Ser
 485 490 495
 Arg Gly Asp Ile Phe Val Val Pro Ala Asn Phe Pro Val Thr Phe Val
 500 505 510
 30 Ala Ser Gln Asn Gln Asn Leu Arg Met Thr Gly Phe Gly Leu Tyr Asn
 515 520 525
 Gln Asn Ile Asn Pro Asp His Asn Gln Arg Ile Phe Val Ala Gly Lys
 530 535 540
 35 Ile Asn His Val Arg Gln Trp Asp Ser Gln Ala Lys Glu Leu Ala Phe
 545 550 555 560
 40 Gly Val Ser Ser Arg Leu Val Asp Glu Ile Phe Asn Ser Asn Pro Gln
 565 570 575
 Glu Ser Tyr Phe Val Ser Arg Gln Arg Gln Arg Ala Ser Glu
 580 585 590

45 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

52

Arg Gln Arg Asp Pro Gln Gln Gln Ala Glu Gln Ala Gln Lys Arg Ala
1 5 10 15

Gln Arg Arg Glu Thr Glu
20

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Pro Arg His Met Gln Ile Ala Gln Gln Arg Ala Glu Arg Arg Ala Glu
1 5 10 15

Lys Glu Lys Arg Lys Gln Gln Lys Arg
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Ala Trp Phe His Val Ser Val Cys Asn Ala Val Phe Val Val Ile
1 5 10 15

Ile Ile Ile Met Leu Leu Met Phe Val Pro Val Val Arg Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGCAGCAGT ATGAGCAGTG

20

5 (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTTTTCGTAK CKKCKTTCGC A

21

20 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACACCATATG CGACAACGTG ATCC

24

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGTTGTTTTTC TCTATTCCTA GGGTTG

26

50 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Gly His His His His His His His His His Ser Ser Gly His
1 5 10 15

Ile Glu Gly Arg His Met
20

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

GGGAATTCCA TATGTATGAG CGTGATCCTC GACAGCAATA CGAGCAATGC CAGAGGCGAT 60
GCGAGTCGGA AGCGACTGAA GAAAGGGAGC 90

(2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAAGCGACTG AAGAAAGGGA GCAAGAGCAG TGTGAACAAC GCTGTGAAAG GGAGTACAAG 60
GAGCAGCAGA GACAGCAATA GGGATCCACA C 91

(2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGAATTCCA TATGCTTCAA AGGCAATACC AGCAATGTCA AGGGCGTTGT CAAGAGCAAC 60
 5 AACAGGGGCA GAGAGAGCAG CAGCAGTGCC AGAGAAAATG C 101

(2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

20 GTGTGGATCC CTAGCTCCTA TTTTTTTTGT GATTATGGTA ATTCTCGTGC TCGCCTCTCT 60
 CTTGTTTCCTT ATATTGCTCC CAGCATTTTC TCTGGCACTG CT 102

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Peanut
- (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Arg Gly Arg Val Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val
 1 5 10 15
 45 Leu Ala Ser Val Ser Ala Thr Gln Ala Lys Ser Pro Tyr Arg Lys Thr
 20 25 30
 Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln Glu Pro
 35 40 45
 50 Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu Glu
 50 55 60
 Tyr Asp Pro Arg Cys Val Tyr Asp Thr Gly Ala Thr Asn Gln Arg His
 55 65 70 75 80

Asp Ile Thr Asn Pro Ile Asn Leu Arg Asp Gly Glu Pro Asp Leu Ser
 390 395 400 405
 5 Asn Asn Phe Gly Arg Leu Phe Glu Val Lys Pro Asp Lys Lys Asn Pro
 410 415 420
 Gln Leu Gln Asp Leu Asp Met Met Leu Thr Cys Val Glu Ile Lys Glu
 425 430 435
 10 Gly Ala Leu Met Leu Pro His Phe Asn Ser Lys Ala Met Val Ile Val
 440 445 450
 Val Val Asn Lys Gly Thr Gly Asn Leu Glu Leu Val Ala Val Arg Lys
 455 460 470
 15 Glu Gln Gln Gln Arg Gly Arg Arg Glu Gln Glu Trp Glu Glu Glu Glu
 480 485 490 500
 20 Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val Arg Arg Tyr Thr
 505 510 515
 Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro Ala Ala His Pro
 520 525 530
 25 Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu Gly Phe Gly Ile
 535 540 545
 Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly Asp Lys Asp Asn
 550 555 560
 30 Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu Ala Phe Pro Gly
 565 570 575 580
 35 Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln Arg Glu Ser His
 585 590 595
 Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Pro Ser Ser Pro Glu Lys
 600 605 610
 40 Glu Asp Gln Glu Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser
 615 620 625
 45 Ile Leu Lys Ala Phe Asn
 630

(2) INFORMATION FOR SEQ ID NO: 22:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Maize

(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Ser Ala Arg Ile Val Val Leu Leu Ala Thr Leu Leu Cys Ala
 1 5 10 15
 Ala Ala Ala Val Ala Ser Ser Trp Glu Asp Asp Asn His His His His
 20 25 30
 Gly Gly His Lys Ser Gly Gln Cys Val Arg Arg Cys Glu Asp Arg Pro
 35 40 45
 Trp His Gln Arg Pro Arg Cys Leu Glu Gln Cys Arg Glu Glu Glu Arg
 50 55 60
 Glu Lys Arg Gln Glu Arg Ser Arg His Glu Ala Asp Asp Arg Ser Gly
 65 70 75 80
 Glu Gly Ser Ser Glu Asp Glu Arg Glu Gln Glu Lys Glu Lys Gln Lys
 85 90 95
 Asp Arg Arg Pro Tyr Val Phe Asp Arg Arg Ser Phe Arg Arg Val Val
 100 105 110
 Arg Ser Glu Gln Gly Ser Leu Arg Val Leu Arg Pro Phe Asp Glu Val
 115 120 125
 Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Val Leu Glu
 130 135 140
 Ala Asn Pro Arg Ser Phe Val Val Pro Ser His Thr Asp Ala His Cys
 145 150 155 160
 Ile Cys Tyr Val Ala Glu Gly Glu Gly Val Val Thr Thr Ile Glu Asn
 165 170 175 180
 Gly Glu Arg Arg Ser Tyr Thr Ile Lys Gln Gly His Val Phe Val Ala
 185 190 195
 Pro Ala Gly Ala Val Thr Tyr Leu Ala Asn Thr Asp Gly Arg Lys Lys
 200 205 210
 Leu Val Ile Thr Lys Ile Leu His Thr Ile Ser Val Pro Gly Glu Phe
 215 220 225
 Gln Phe Phe Phe Gly Pro Gly Gly Arg Asn Pro Glu Ser Phe Leu Ser
 230 235 240 245
 Ser Phe Ser Lys Ser Ile Gln Arg Ala Ala Tyr Lys Thr Ser Ser Asp
 250 255 260
 Arg Leu Glu Arg Leu Phe Gly Arg His Gly Gln Asp Lys Gly Ile Ile

265 270 275

Val Arg Ala Thr Glu Glu Gln Thr Arg Glu Leu Arg Arg His Ala Ser
280 285 290

5 Glu Gly Gly His Gly Pro His Trp Pro Leu Pro Pro Phe Gly Glu Ser
295 300 305

Arg Gly Pro Tyr Ser Leu Leu Asp Gln Arg Pro Ser Ile Ala Asn Gln
10 310 315 320 325

His Gly Gln Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Asp Leu Ala
330 335 340

15 Glu His Asp Val Ser Val Ser Phe Ala Asn Ile Thr Ala Gly Ser Met
345 350 355

Ser Ala Pro Leu Phe Asn Thr Arg Ser Phe Lys Ile Ala Tyr Val Pro
360 365 370

20 Asn Gly Lys Gly Tyr Ala Glu Ile Val Cys Pro His Arg Gln Ser Gln
375 380 385

Gly Gly Glu Ser Glu Arg Glu Arg Asp Lys Gly Arg Arg Ser Glu Glu
25 390 395 400 405

Glu Glu Glu Glu Ser Ser Glu Glu Gln Glu Glu Ala Gly Gln Gly Tyr
410 415 420

30 His Thr Ile Arg Ala Arg Leu Ser Pro Gly Thr Ala Phe Val Val Pro
425 430 435

Ala Gly His Pro Phe Val Ala Val Ala Ser Arg Asp Ser Asn Leu Gln
440 445 450

35 Ile Val Cys Phe Glu Val His Ala Asp Arg Asn Glu Lys Val Phe Leu
455 460 470

Ala Gly Ala Asp Asn Val Leu Gln Lys Leu Asp Arg Val Ala Lys Ala
40 480 485 490 500

Leu Ser Phe Ala Ser Lys Ala Glu Glu Val Asp Glu Val Leu Gly Ser
505 510 515

45 Arg Arg Glu Lys Gly Phe Leu Pro Gly Pro Glu Glu Ser Gly Gly His
520 525 530

Glu Glu Arg Glu Gln Glu Glu Glu Glu Arg Glu Glu Arg His Gly Gly
535 540 545

50 Arg Gly Glu Arg Glu Arg His Gly Arg Glu Glu Arg Glu Lys Glu Glu
550 555 560

Glu Arg Glu Gly Arg His Gly Gly Arg Glu Glu Arg Glu Glu Glu Glu
55 565 570 575 580

Met Val Thr Ala Arg Met
5 600

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Gly Gln Pro Trp Glu Thr Gln Glu Cys Met Arg Arg Cys Arg Arg Arg
20 25 30

Gly

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Barley
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Thr Ser Leu Leu Phe Ala Ala Ala Val Ser Ala Ser His Asp Asp Glu
20 25 30

55 Asp Asp Arg Arg Gly Gly His Ser Leu Gln Gln Cys Val Gln Arg Cys
 35 40 45

Arg Gln Glu Arg Pro Arg Tyr Ser His Ala Arg Cys Val Gln Glu Cys
50 55 60

5 Arg Asp Asp Gln Gln Gln His Gly Arg His Glu Gln Glu Glu Glu Gln
65 70 75 80

Gly Arg Gly Arg Gly Trp His Gly Glu Gly Glu Arg Glu Glu Glu His
85 90 95

10 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu His
100 105 110

15 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
115 120 125

Gly Arg Gly His Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
130 135 140

20 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Glu
145 150 155 160

Gly Arg Gly Arg Gly Arg Arg Gly Glu Gly Glu Arg Asp Glu Glu Gln
165 170 175 180

25 Gly Asp Ser Arg Arg Pro Tyr Val Phe Gly Pro Arg Ser Phe Arg Arg
185 190 195

30 Ile Ile Gln Ser Asp His Gly Phe Val Arg Ala Leu Arg Pro Phe Asp
200 205 210

Gln Val Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Ile
215 220 225

35 Met Glu Val Asn Pro Arg Ala Phe Val Val Pro Gly Phe Thr Asp Ala
230 235 240 245

Asp Gly Val Gly Tyr Val Ala Gln Gly Glu Gly Val Leu Thr Val Ile
250 255 260

40 Glu Asn Gly Glu Lys Arg Ser Tyr Thr Val Lys Glu Gly Asp Val Ile
265 270 275

45 Val Ala Pro Ala Gly Ser Ile Met His Leu Ala Asn Thr Asp Gly Arg
280 285 290

Arg Lys Leu Val Ile Ala Lys Ile Leu His Thr Ile Ser Val Pro Gly
295 300 305

50 Lys Phe Gln Phe Leu Ser Val Lys Pro Leu Leu Ala Ser Leu Ser Lys
310 315 320 325

Arg Val Leu Arg Ala Ala Phe Lys Thr Ser Asp Glu Arg Leu Glu Arg
330 335 340

55 Leu Phe Asn Gln Arg Gln Gly Gln Glu Lys Thr Arg Ser Val Ser Ile

345 350 355
 Val Arg Ala Ser Glu Glu Gln Leu Arg Glu Leu Arg Arg Glu Ala Ala
 360 365 370
 5
 Glu Gly Gly Gln Gly His Arg Trp Pro Leu Pro Pro Phe Arg Gly Asp
 375 380 385
 10
 Ser Arg Asp Thr Phe Asn Leu Leu Glu Gln Arg Pro Lys Ile Ala Asn
 390 395 400 405
 Arg His Gly Arg Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Ala Leu
 410 415 420
 15
 Ala Asn Gln Asp Val Arg Val Ala Val Ala Asn Ile Thr Pro Gly Ser
 425 430 435
 Met Thr Ala Pro Tyr Leu Asn Thr Gln Ser Phe Lys Leu Ala Val Val
 440 445 450
 20
 Leu Glu Gly Glu Gly Glu Val Gln Ile Val Cys Pro His Leu Gly Arg
 455 460 470
 25
 Glu Ser Glu Ser Glu Arg Glu His Gly Lys Gly Arg Arg Arg Glu Glu
 480 485 490 500
 Glu Glu Asp Asp Gln Arg Gln Gln Arg Arg Arg Gly Ser Glu Ser Glu
 505 510 515
 30
 Ser Glu Glu Glu Glu Glu Gln Gln Arg Tyr Glu Thr Val Arg Ala Arg
 520 525 530
 Val Ser Arg Gly Ser Ala Phe Val Val Pro Pro Gly His Pro Val Val
 535 540 545
 35
 Glu Ile Ser Ser Ser Gln Gly Ser Ser Asn Leu Gln Val Val Cys Phe
 550 555 560
 40
 Glu Ile Asn Ala Glu Arg Asn Glu Arg Val Trp Leu Ala Gly Arg Asn
 565 570 575 580
 Asn Val Ile Gly Lys Leu Gly Ser Pro Ala Gln Glu Leu Thr Phe Gly
 585 590 595
 45
 Arg Pro Ala Arg Glu Val Gln Glu Val Phe Arg Ala Gln Asp Gln Asp
 600 605 610
 Glu Gly Phe Val Ala Gly Pro Glu Gln Gln Ser Arg Glu Gln Glu Gln
 615 620 625
 50
 Glu Gln Glu Arg His Arg Arg Arg Gly Asp Arg Gly Arg Gly Asp Glu
 630 635 640
 55
 Ala Val Glu Thr Phe Leu Arg Met Ala Thr Gly Ala Ile
 645 650 655

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Soybean (Glycine max)
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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Met Met Arg Ala Arg Phe Pro Leu Leu Leu Leu Gly Leu Val Phe Leu
1          5          10          15
Ala Ser Val Ser Val Ser Phe Gly Ile Ala Tyr Trp Glu Lys Glu Asn
20         20         25         30
Pro Lys His Asn Lys Cys Leu Gln Ser Cys Asn Ser Glu Arg Asp Ser
25        35        40        45
Tyr Arg Asn Gln Ala Cys His Ala Arg Cys Asn Leu Leu Lys Val Glu
50        55        60
Lys Glu Glu Cys Glu Glu Gly Glu Ile Pro Arg Pro Arg Pro Arg Pro
30       65       70       75       80
Gln His Pro Glu Arg Glu Pro Gln Gln Pro Gly Glu Lys Glu Glu Asp
35          85          90          95
Glu Asp Glu Gln Pro Arg Pro Ile Pro Phe Pro Arg Pro Gln Pro Arg
100        105        110
Gln Glu Glu Glu His Glu Gln Arg Glu Glu Gln Glu Trp Pro Arg Lys
40        115        120        125
Glu Glu Lys Arg Gly Glu Lys Gly Ser Glu Glu Glu Asp Glu Asp Glu
130        135        140
Asp Glu Glu Gln Asp Glu Arg Gln Phe Pro Phe Pro Arg Pro Pro His
45       145       150       155       160
Gln Lys Glu Glu Arg Asn Glu Glu Glu Asp Glu Asp Glu Glu Gln Gln
50       165       170       175       180
Arg Glu Ser Glu Glu Ser Glu Asp Ser Glu Leu Arg Arg His Lys Asn
185        190        195
Lys Asn Pro Phe Leu Phe Gly Ser Asn Arg Phe Glu Thr Leu Phe Lys
55       200       205       210

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64

Asn Gln Tyr Gly Arg Ile Arg Val Leu Gln Arg Phe Asn Gln Arg Ser
 215 220 225
 5 Pro Gln Leu Gln Asn Leu Arg Asp Tyr Arg Ile Leu Glu Phe Asn Ser
 230 235 240 245
 Lys Pro Asn Thr Leu Leu Leu Pro Asn His Ala Asp Ala Asp Tyr Leu
 250 255 260
 10 Ile Val Ile Leu Asn Gly Thr Ala Ile Leu Ser Leu Val Asn Asn Asp
 265 270 275
 Asp Arg Asp Ser Tyr Arg Leu Gln Ser Gly Asp Ala Leu Arg Val Pro
 280 285 290
 15 Ser Gly Thr Thr Tyr Tyr Val Val Asn Pro Asp Asn Asn Glu Asn Leu
 295 300 305
 Arg Leu Ile Thr Leu Ala Ile Pro Val Asn Lys Pro Gly Arg Phe Glu
 310 315 320 325
 Ser Phe Phe Leu Ser Ser Thr Glu Ala Gln Gln Ser Tyr Leu Gln Gly
 330 335 340
 25 Phe Ser Arg Asn Ile Leu Glu Ala Ser Tyr Asp Thr Lys Phe Glu Glu
 345 350 355
 Ile Asn Lys Val Leu Phe Ser Arg Glu Glu Gly Gln Gln Gln Gly Glu
 360 365 370
 30 Gln Arg Leu Gln Glu Ser Val Ile Val Glu Ile Ser Lys Glu Gln Ile
 375 380 385
 Arg Ala Leu Ser Lys Arg Ala Lys Ser Ser Ser Arg Lys Thr Ile Ser
 390 395 400 405
 Ser Glu Asp Lys Pro Phe Asn Leu Arg Ser Arg Asp Pro Ile Tyr Ser
 410 415 420
 40 Asn Lys Leu Gly Lys Phe Phe Glu Ile Thr Pro Glu Lys Asn Pro Gln
 425 430 435
 Leu Arg Asp Leu Asp Ile Phe Leu Ser Ile Val Asp Met Asn Glu Gly
 440 445 450
 45 Ala Leu Leu Leu Pro His Phe Asn Ser Lys Ala Ile Val Ile Leu Val
 455 460 470
 Ile Asn Glu Gly Asp Ala Asn Ile Glu Leu Val Gly Leu Lys Glu Gln
 480 485 490 500
 Gln Gln Glu Gln Gln Gln Glu Glu Gln Pro Leu Glu Val Arg Lys Tyr
 505 510 515
 55 Arg Ala Glu Leu Ser Glu Gln Asp Ile Phe Val Ile Pro Ala Gly Tyr
 520 525 530

Pro Val Val Val Asn Ala Thr Ser Asn Leu Asn Phe Phe Ala Ile Gly
535 540 545

5 Ile Asn Ala Glu Asn Asn Gln Arg Asn Phe Leu Ala Gly Ser Gln Asp
550 555 560

Asn Val Ile Ser Gln Ile Pro Ser Gln Val Gln Glu Leu Ala Phe Pro
565 570 575 580

Gly Ser Ala Gln Ala Val Glu Lys Leu Leu Lys Asn Gln Arg Glu Ser
585 590 595

15 Tyr Phe Val Asp Ala Gln Pro Lys Lys Lys Glu Glu Gly Asn Lys Gly
600 605 610

Arg Lys Gly Pro Leu Ser Ser Ile Leu Arg Ala Phe Tyr
615 620 625

20

(2) INFORMATION FOR SEQ ID NO: 26:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Lys Glu Asp His Gln Phe Glu Thr Arg Gly Glu Ile Leu Glu Cys
1 5 10 15

40

Tyr Arg Leu Cys Gln Gln Gln
20

45

(28) INFORMATION FOR SEQ ID NO: 27:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Gln Lys His Arg Ser Gln Ile Leu Gly Cys Tyr Leu Xxx cys Gln Gln
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenocarpus sinuatus*

(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Leu Asp Pro Ile Arg Gln Gln Gln Leu Cys Gln Met Arg Cys Gln Gln
1 5 10 15

Gln Glu Lys Asp Pro Arg Gln Gln Gln Gln Cys Lys
20 25